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## Genetic variability, heritability and genetic advance in rice (*Oryza sativa* L.) under salt stressed soil.

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### Abstract

The present investigation was laid out during kharif season of 2014 at Research farm of Genetics and Plant Breeding Department, N.D. University of Agriculture and Technology. It comprised 22 parents (19 lines and 3 testers) along with 57 F<sub>1</sub> hybrid grown in Randomized Block Design with three replications. Total 15 quantitative traits viz., days to 50 % flowering, plant height (cm), flag leaf area, (cm<sup>2</sup>), panicle bearing tillers per plant, panicle length (cm), spikelets per panicle, grains per panicle, spikelet fertility (%), biological yield per plant (g), harvest index (%), L:B ratio, 1000-grains wt. (g) Kernel length (mm), Kernel width (mm) and grain yield per plant (g) were used for evaluation under salt affected soil. Analysis of variance indicated the existence of significant genotypic differences among the parents and their hybrids for the yield, its components for all the characters. High estimates of GCV and PCV values were observed for flag leaf area and panicle bearing tillers per plant. High heritability coupled with high genetic advance as per cent of mean was observed for flag leaf area, grains per panicle, panicle bearing tillers per plant, spikelet per panicle, and plant height which indicated that these traits were controlled by additive type of gene action. The remaining traits were mostly under the influence of nonadditive gene effects as they recorded low to moderate estimates of genetic advance. It is concluded that, emphasis should be given to select these quantitative traits to enhance the yield potential of rice (*Oryza sativa* L.) under salt affected soil.

**Keywords:** rice, GCV, PCV, heritability, genetic advance

### Introduction

Rice (*Oryza sativa* L.) is an important cereal crop meeting the feeding requirement of more than one third of the world's population. It is grown under diverse agroclimatic conditions and over wide geographical range (Cheng *et al.*, 2005) [6]. With present scenario of increasing population global rice requirement by the year 2020 is estimated to be around 122 million tons as against the present production of about 100 million tons, thus leaving a gap of about 22 million tons rice. Salinity stress is one of the major abiotic constraints which limits rice production and it is estimated that 20% of all cultivated land and nearly half of irrigated land is affected by salt, greatly reducing the yield of crops to well below their genetic potential. One of the possible way to improve crop production under salt stress soil is through critical analysis of genetic variation governing the yield related quantitative traits. The success of any breeding programme depends on quantum of genetic variability present in the available genetic stocks (Basavaraja *et al.*, 2013) [6] and the extent to which various traits are heritable. The heritability estimates determine the portion of total variation which is transferred from parent to their offspring which is important for successful selection in crop improvement. The heritability when combined with genetic advance helps in predicting the genetic gain which could be achieved through selection. Therefore, the present study was undertaken to determine the extent of variability, heritability and genetic advance present in rice for 15 quantitative traits under salt affected soil

### Material and Method

The present experiment was conducted at Research Farm of Department of Genetics and Plant Breeding, N.D. University of Agriculture and Technology, Kumarganj, Faizabad. The experimental material consisted 22 parental lines and 57 F<sub>1</sub> hybrids grown in Randomized block design during kharif season of 2014. The 57 hybrids were obtained through crossing 19 lines with three testers (22 parents) i.e., Narendra 359, Sarjoo 52 and Narendra Usar-3 in line x tester manner. All the recommended package of practices was followed and need based plant protection was done. Observations on 15 morphological and quality characters were recorded based on ten randomly selected plants in each genotype in each replication.

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The traits were days to 50 % flowering, plant height (cm), flag leaf area, (cm<sup>2</sup>), panicle bearing tillers per plant, panicle length (cm), spikelets per panicle, grains per panicle, spikelet fertility (%), biological yield per plant (g), harvest index (%), L:B ratio, 1000-grains wt. (g) Kernel length (mm), Kernel width (mm) and grain yield per plant (g). Analysis of variance was done based on RBD (Panse and Sukhatme, 1961) for each of the characters separately. The phenotypic and genotypic coefficient of variance, heritability in broad sense (Burton and Devane, 1953) [5] and Genetic advance was estimated (Allard, 1960) [1].

### Result and Discussion

Presence of genetic variability is pre-requisite for selection of superior genotypes during crop improvement programme. Therefore, assessment of extent of variation present in the genetic material is important to estimate the magnitude of improvement that can be achieved in breeding material for various characters. The analysis of variance indicated highly significant mean sum of squares due to treatment for all the 15 characters at 1% level of significance (Table 1). This reveals high variability among the genotypes providing ample scope of selection for different quantitative traits under salt affected soil. Significant variation for various quantitative traits were also reported by Bekele *et al.*, (2013) [4], Nilman *et al.*, (2014) and Sandhya *et al.*, (2015) [16].

Estimates of phenotypic variances were higher than genotypic variance for all the studied quantitative traits indicating the influence of environmental factors on these traits. Highest phenotypic and genotypic variances were observed for spikelets per panicle (874.96, 857.49) and grains per panicle (752.45, 741.97) followed by plant height (93.95, 92.49) and flag leaf area (74.50, 72.78) (Table 2). Therefore, selection of desirable genotypes in breeding programme for these traits is favourable. Anjaneyulu *et al.*, (2010) [2] and Idris (2012) [8] also observed similar results during their experiment in rice. In the present study it was found that there is close correspondence of genotypic variance to phenotypic variance for most of the traits specifying that phenotypic variability is a reliable measure of genotypic variability.

Coefficient of variation estimates i.e. GCV and PCV revealed that phenotypic coefficient of variation (PCV) was slightly higher than genotypic coefficient of variation (GCV) for all the studied traits revealing very less influence of environment on the expression of traits and selection through phenotype alone could be successful. High estimates of GCV and PCV (> 20%) was recorded for flag leaf area (27.84, 28.17) and panicle bearing tillers per plant (20.59, 21.28) indicating large scope of selection for these characters, while other characters had moderate (10-20%) or low GCV and PCV values indicating less variability and need for creation of variation through hybridization and mutation in salt stress soil. Limbani *et al.*, (2017) [10] and Prasad *et al.*, (2017) also observed close estimates of GCV and PCV for different traits in rice and values of PCV were slightly higher than GCV.

Coefficient of variations measures the amount of variability

present in the characters but it alone is not sufficient to determine the expected progress that could be made in quantitative traits (Falconer, 1981) [7]. It has been suggested that estimates of GCV and heritability together provide a better portrait of amount of genetic gain expected under phenotypic selection (Burton and Devane, 1953) [5]. Heritability is a useful quantitative parameter, which considers the role of heredity and environment determining the expression of a trait (Allard, 1960) [1]. In the present study, high estimates of heritability in broad sense (>75%) was observed for almost all the traits except spikelet fertility, harvest index and kernel width, which exhibited moderate heritability (50-75%). Similar observation were made by Padmaja *et al.*, (2008) and Sumanth *et al.*, (2017) [17] having high heritability for various quantitative traits in rice.

The genetic advance is a useful indicator of the progress that can be expected as a result of exercising selection (Vanniarajan *et al.*, 1996) [19]. Since it is dependent on phenotypic variability and heritability in addition to selection intensity, the heritability estimates in conjunction with genetic advance will be more effective and reliable in predicting the response to selection (Johnson *et al.*, 1955) [9]. Genetic advance in percent mean was observed highest (>20%) for flag leaf area followed by grains per panicle, panicle bearing tillers per plant, spikelet per panicle, biological yield per panicle, L: B ratio and plant height. On the other hand, moderate genetic advance (10-20%) was observed for kernel length, panicle length, 1000 grain weight, grain yield per plant and kernel width. Neeta *et al.* (2018) also reported high genetic advance in percent mean for flag leaf area, panicle bearing tillers per plant, spikelets per panicle, biological yield per plant and L: B ratio under salt stressed soil.

In general, characters having high heritability coupled with high genetic advance are controlled by additive gene action (Patil *et al.*, 2003) [13] and can be improved through simple method of selections. The characters showing high heritability along with moderate or low genetic advance can be improved by intermating superior genotypes of segregating population developed from combination breeding (Samadia, 2005) [15].

### Conclusion

In the present experiment, considering the evaluation of important variability parameters i.e. Coefficient of variation, heritability and genetic advance together, it was revealed that flag leaf area, grains per panicle, panicle bearing tillers per plant, spikelet per panicle and plant height are most important characters because they have high heritability coupled with high genetic advance. This indicates involvement of additive gene in controlling gene responsible for these traits. Therefore, these characters could be improved through selection in segregating generations. The traits with high heritability and low genetic advance e.g. days to 50% fertility, spikelet fertility and harvest index indicated that they are governed by non-additive action and can be improved by intermating superior genotypes of segregating population developed from combination breeding

**Table 1:** Analysis of variance for randomized block design for 15 characters in rice

Characters	Sources of variation		
	Replications	Treatments	Error
d.f.	2	78	156
Days to 50% flowering	0.13	55.23**	1.06
Plant height (cm)	1.27	278.92**	1.46
Flag leaf area (cm <sup>2</sup> )	2.71	220.04**	1.72
Panicle bearing tillers per plant	0.04	10.88**	0.24

Panicle length (cm)	0.11	13.38**	0.62
Spikelets per panicle	10.61	2589.93**	17.46
Grains per panicle	2.32	2236.38**	10.48
Spikelet fertility (%)	0.30	45.37**	5.69
1000- grains weight (g)	0.08	12.37**	0.47
Biological yield per plant (g)	3.06	121.16**	2.35
Harvest-index (%)	4.49	12.31**	1.38
Kernel length (mm)	0.07	1.10**	0.02
Kernel width (mm)	0.00	0.11**	0.01
L:B ratio	0.01	0.37**	0.02
Grains yield per plant(g)	1.44	23.15**	0.66

**Table 2:** Estimates of general mean, phenotypic (PCV) and genotypic (GCV) coefficient of variation, heritability in broad sense ( $h^2_b$ ) and genetic advance in per cent of mean for 15 characters in rice

Characters	mean	$\delta^2_g$	$\delta^2_p$	Coefficient of variation (%)		Heritability in broad sense (%)	Genetic advance in per cent of mean
				PCV	GCV		
Days to 50% flowering	98.78	18.06	19.12	4.42	4.30	94.44	8.61
Plant height (cm)	92.47	92.49	93.95	10.48	10.39	98.44	21.25
Flag leaf area (cm <sup>2</sup> )	30.63	72.78	74.50	28.17	27.84	97.69	56.69
Panicle bearing tillers per plant	9.14	3.55	3.79	21.28	20.59	93.66	41.06
Panicle length (cm)	22.82	4.25	4.87	9.67	9.03	87.26	17.38
Spikelets per panicle	157.03	857.49	874.96	18.83	18.64	98.00	38.02
Grains per panicle	132.32	741.96	752.45	20.72	20.58	98.61	42.10
Spikelet fertility (%)	84.14	13.23	18.92	5.16	4.32	69.91	7.44
1000- grains weight (g)	23.59	3.97	4.44	8.92	8.43	89.38	16.43
Biological yield per plant (g)	50.93	39.60	41.96	12.71	12.35	94.39	24.72
Harvest-index (%)	41.07	3.64	5.03	5.45	4.64	72.45	8.14
Kernel length (mm)	6.40	0.36	0.39	9.70	9.37	93.43	18.67
Kernel width (mm)	2.30	0.03	0.05	9.21	7.38	72.35	13.72
L:B ratio	2.79	0.12	0.14	13.33	12.19	83.72	22.99
Grains yield per plant(g)	20.93	7.49	8.16	13.64	13.07	91.81	15.81

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